Resource Summary Report

Generated by RRID on Aug 5, 2026

Genomic HyperBrowser

RRID:SCR_010909
Type: Tool

Proper Citation

Genomic HyperBrowser (RRID:SCR_010909)

Resource Information

URL: http://hyperbrowser.uio.no/hb/

Proper Citation: Genomic HyperBrowser (RRID:SCR_010909)

Description: A generic web-based system, providing statistical methodology and computing power to handle a variety of biological inquires on genomic datasets.

Abbreviations: Genomic HyperBrowser

Synonyms: The Genomic HyperBrowser

Resource Type: data analysis service, analysis service resource, production service resource, service resource

Defining Citation: PMID:23632163, PMID:21182759

Keywords: genomic, genomic track, gene regulation, disease association, epigenetic modification, genome

Resource Name: Genomic HyperBrowser

Resource ID: SCR_010909

Alternate IDs: OMICS_00638

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260805T044249+0000

Ratings and Alerts

No rating or validation information has been found for Genomic HyperBrowser.

No alerts have been found for Genomic HyperBrowser.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Fan Q, et al. (2020) LXR? Regulates ChREBP? Transactivity in a Target Gene-Specific Manner through an Agonist-Modulated LBD-LID Interaction. Cells, 9(5).

Bonnefont J, et al. (2019) Cortical Neurogenesis Requires Bcl6-Mediated Transcriptional Repression of Multiple Self-Renewal-Promoting Extrinsic Pathways. Neuron, 103(6), 1096.

Sun Z, et al. (2018) Transcription-associated histone pruning demarcates macroH2A chromatin domains. Nature structural & molecular biology, 25(10), 958.

Kanduri C, et al. (2017) Genome build information is an essential part of genomic track files. Genome biology, 18(1), 175.

Simovski B, et al. (2017) GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. GigaScience, 6(7), 1.

Romasko EJ, et al. (2016) Male-Specific Transcription Factor Occupancy Alone Does Not Account for Differential Methylation at Imprinted Genes in the mouse Germ Cell Lineage. G3 (Bethesda, Md.), 6(12), 3975.

Handel AE, et al. (2016) Bioinformatics Analysis of Estrogen-Responsive Genes. Methods in molecular biology (Clifton, N.J.), 1366, 29.

Saleh S, et al. (2016) HIV integration and the establishment of latency in CCL19-treated resting CD4(+) T cells require activation of NF-?B. Retrovirology, 13(1), 49.

Lercher L, et al. (2015) Generation of a synthetic GlcNAcylated nucleosome reveals regulation of stability by H2A-Thr101 GlcNAcylation. Nature communications, 6, 7978.

Kocer A, et al. (2015) Oxidative DNA damage in mouse sperm chromosomes: Size matters. Free radical biology & medicine, 89, 993.

Ricigliano VA, et al. (2015) EBNA2 binds to genomic intervals associated with multiple sclerosis and overlaps with vitamin D receptor occupancy. PloS one, 10(4), e0119605.

Mosquera Orgueira A, et al. (2015) Hidden among the crowd: differential DNA methylation-expression correlations in cancer occur at important oncogenic pathways. Frontiers in genetics, 6, 163.

Bengtsen M, et al. (2015) c-Myb Binding Sites in Haematopoietic Chromatin Landscapes. PloS one, 10(7), e0133280.

Rydbeck H, et al. (2015) ClusTrack: feature extraction and similarity measures for clustering of genome-wide data sets. PloS one, 10(4), e0123261.

Watson CT, et al. (2015) Sequencing of the human IG light chain loci from a hydatidiform mole BAC library reveals locus-specific signatures of genetic diversity. Genes and immunity, 16(1), 24.

Ragoczy T, et al. (2014) Functional redundancy in the nuclear compartmentalization of the late-replicating genome. Nucleus (Austin, Tex.), 5(6), 626.

Watson CT, et al. (2012) Age-associated hyper-methylated regions in the human brain overlap with bivalent chromatin domains. PloS one, 7(9), e43840.

Kresse SH, et al. (2012) Integrative analysis reveals relationships of genetic and epigenetic alterations in osteosarcoma. PloS one, 7(11), e48262.

Disanto G, et al. (2012) Vitamin D receptor binding, chromatin states and association with multiple sclerosis. Human molecular genetics, 21(16), 3575.

Disanto G, et al. (2012) Genomic regions associated with multiple sclerosis are active in B cells. PloS one, 7(3), e32281.